

FIG. 1

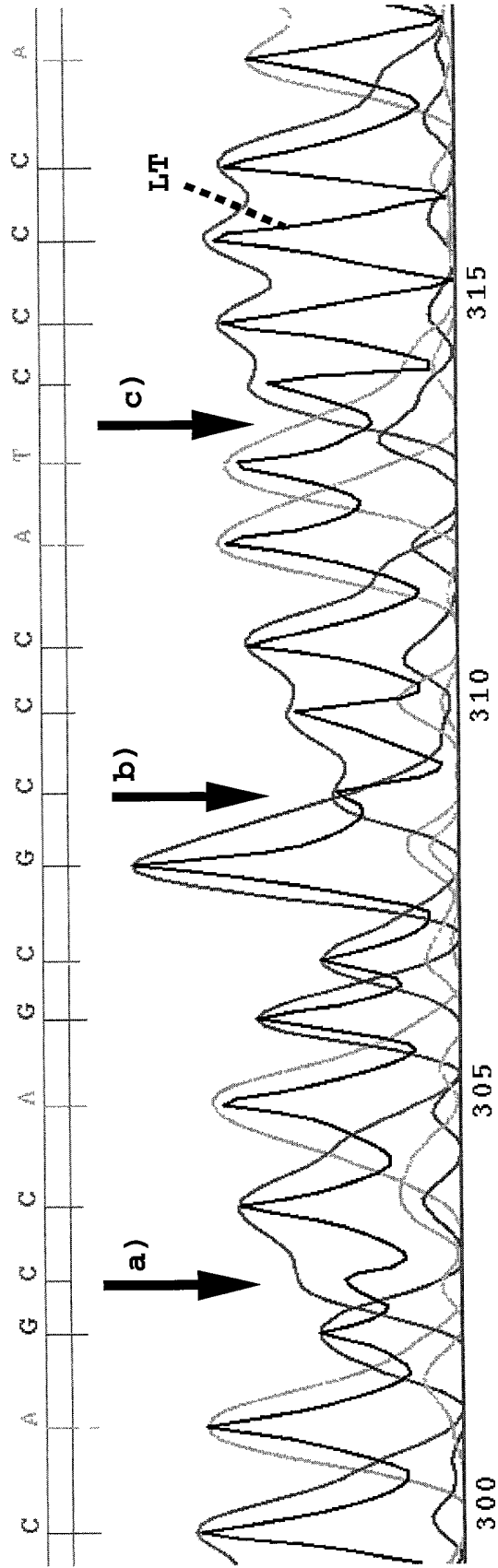


FIG. 2

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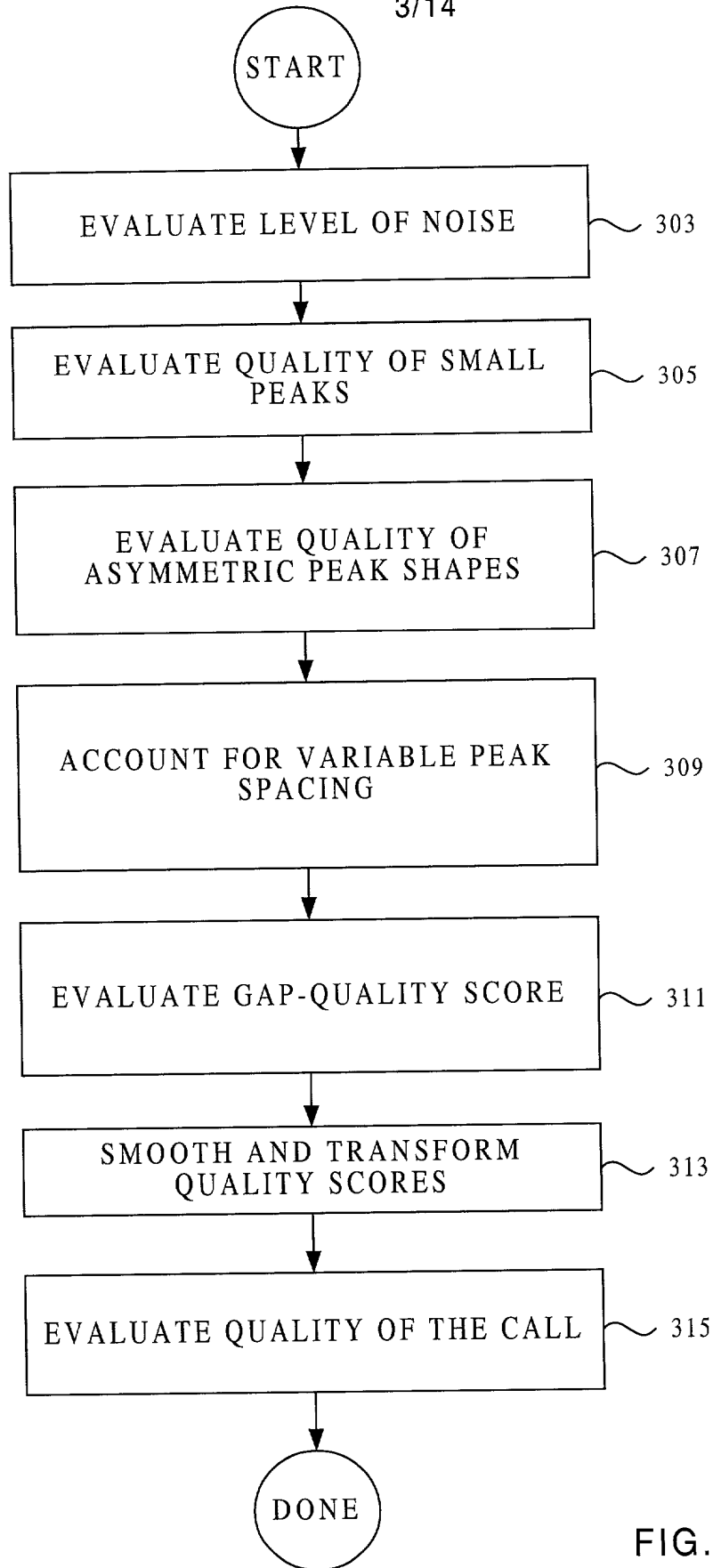
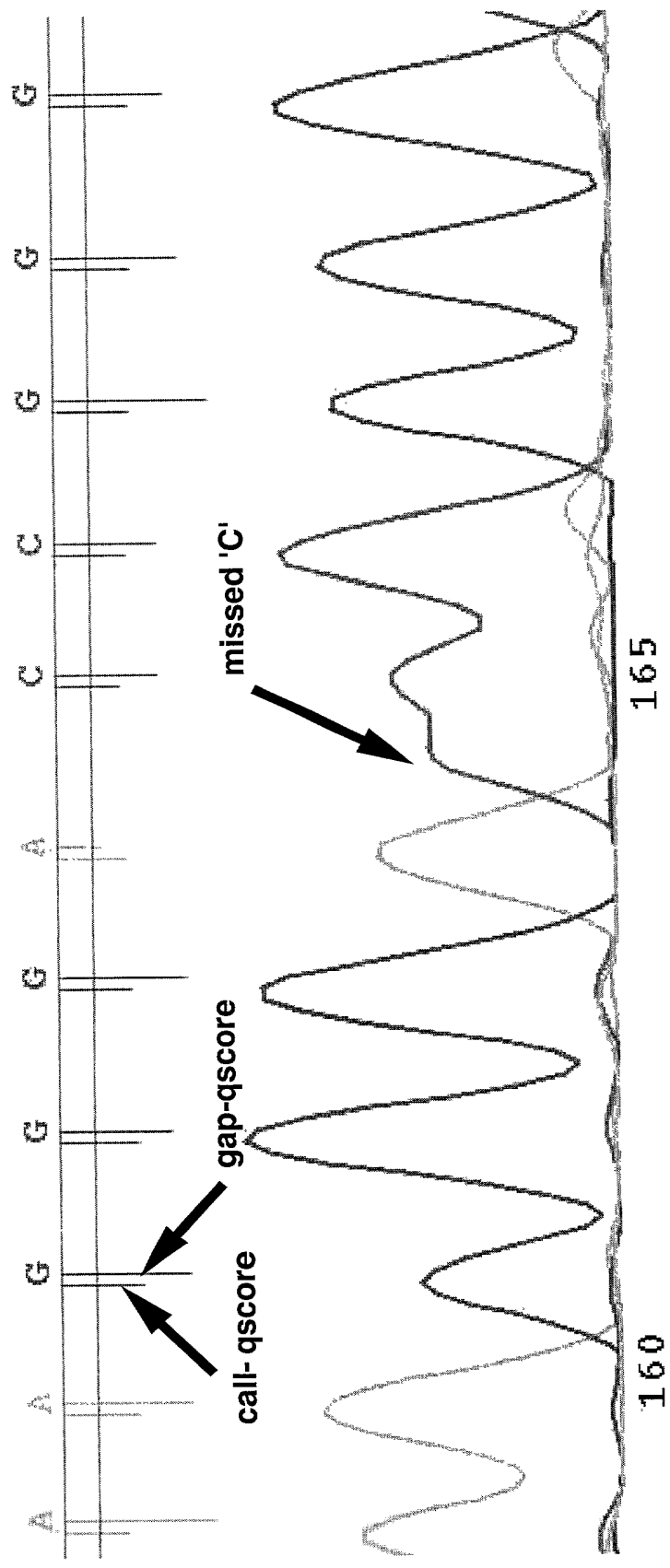


FIG. 3



AAGGGACCCGGG true sequence

alignment alternatives:

AACGGACCC-GGG

AACGGAC-CCGGG

AACGGA-CCGGG correct alignment

FIG. 4

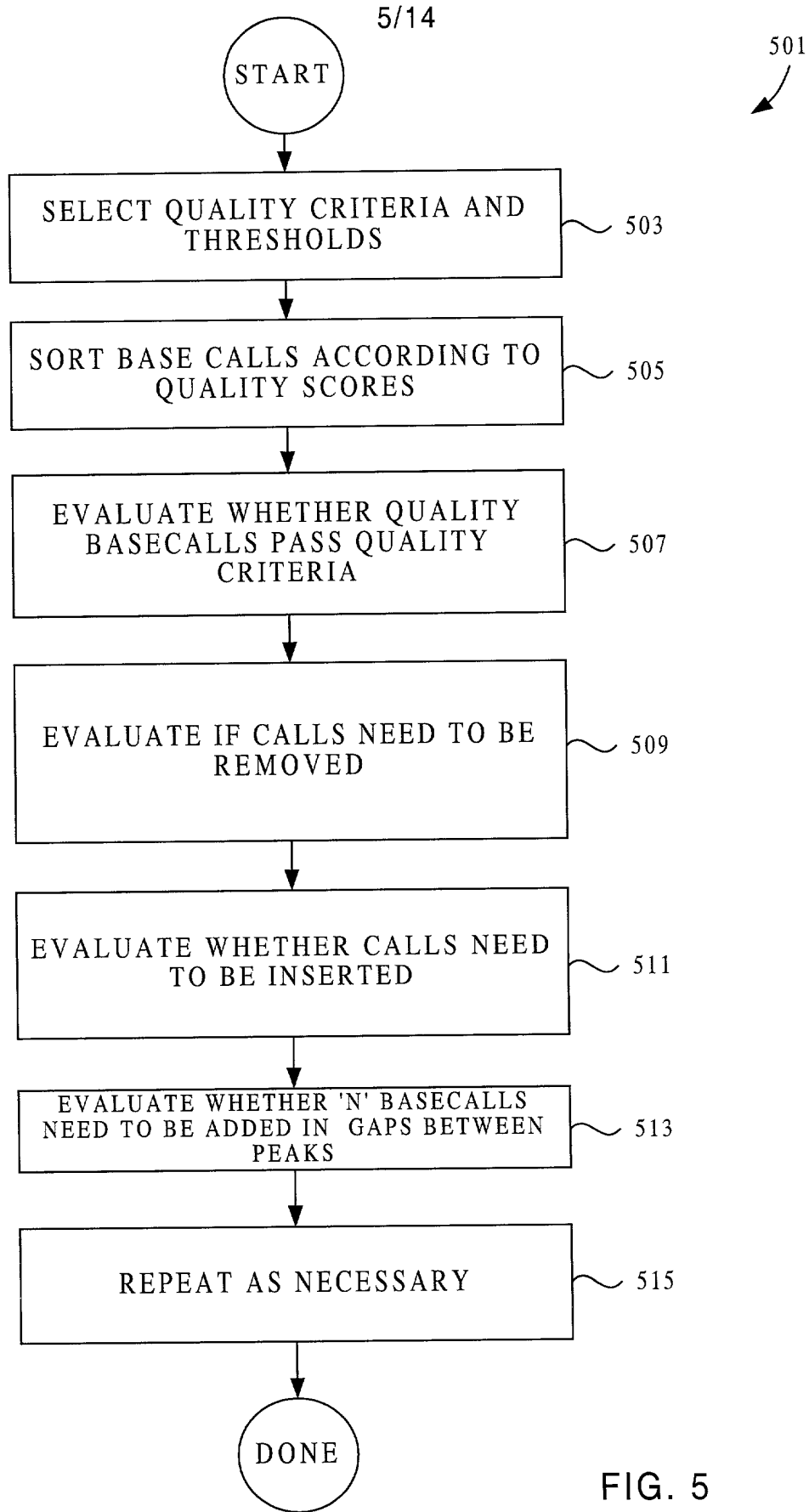


FIG. 5

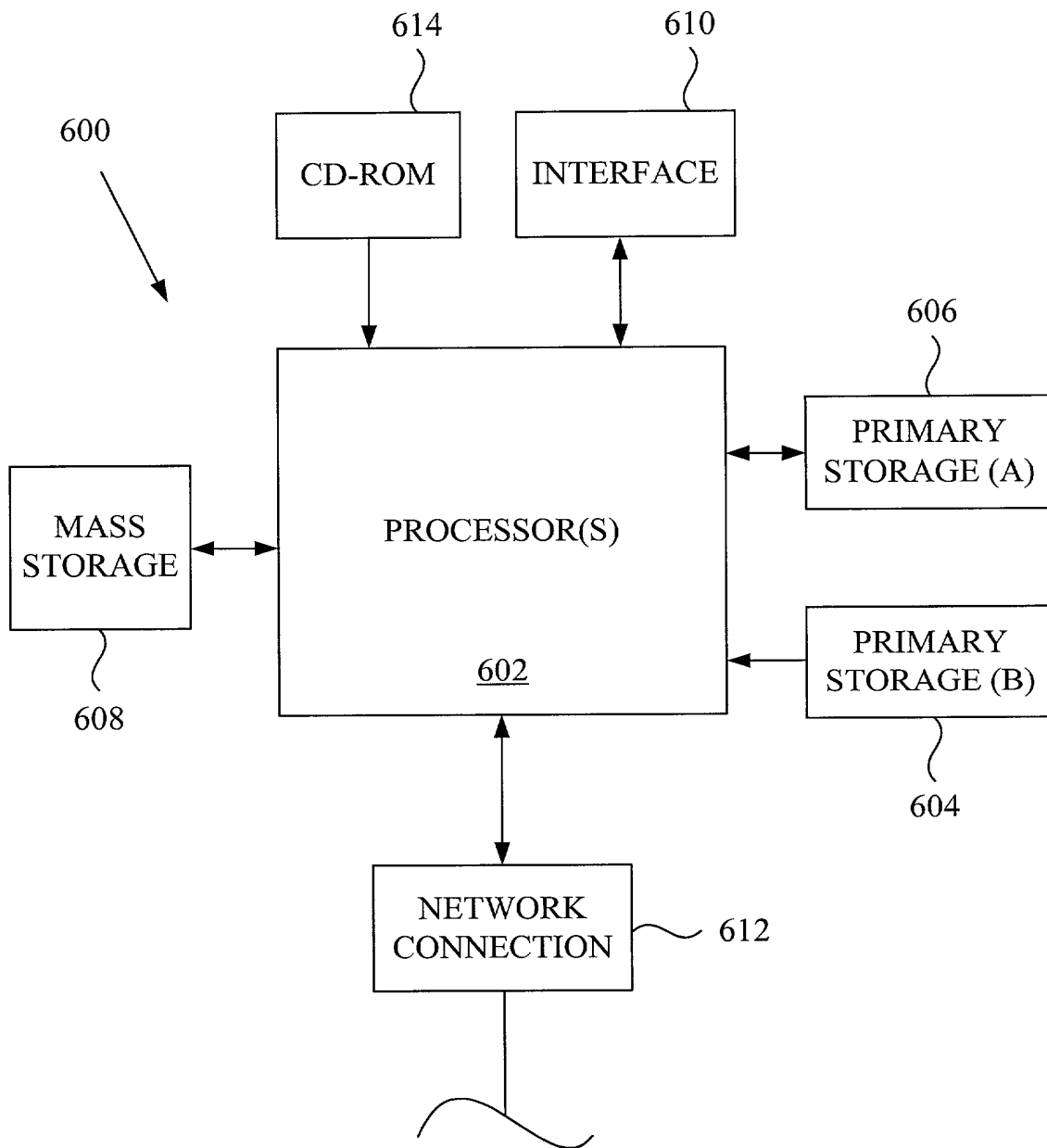


FIG. 6

MB_prim

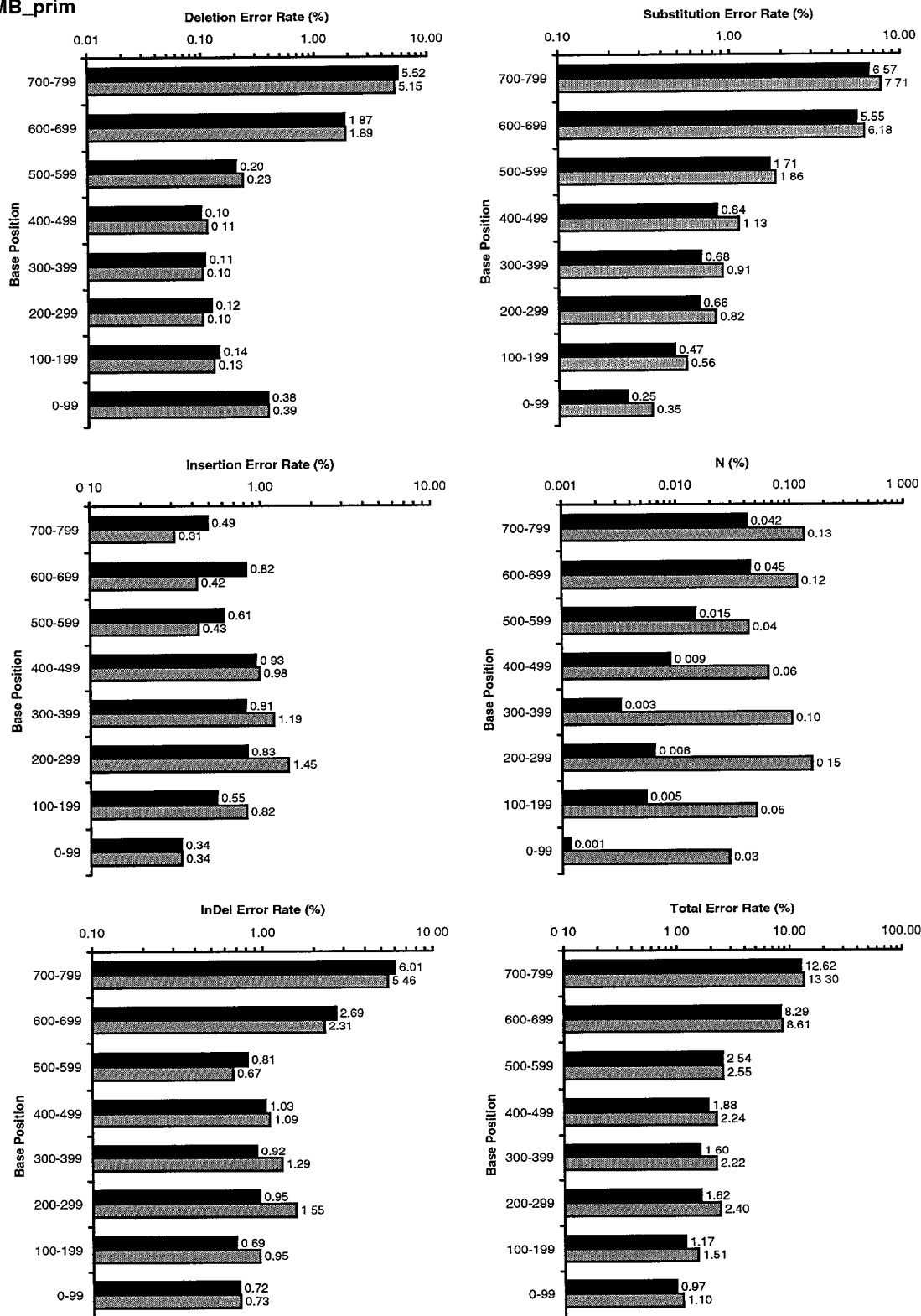


FIG. 7A

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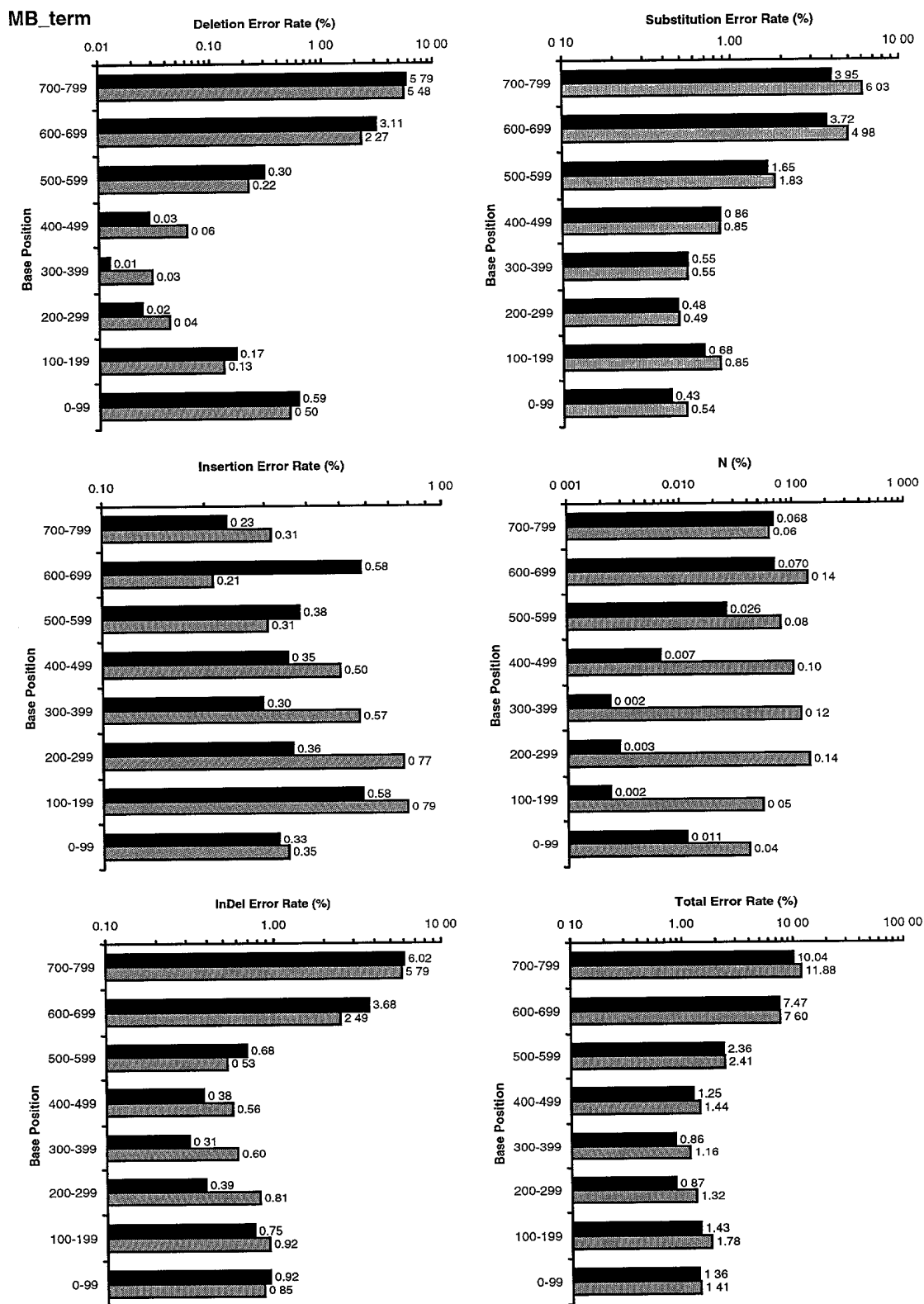


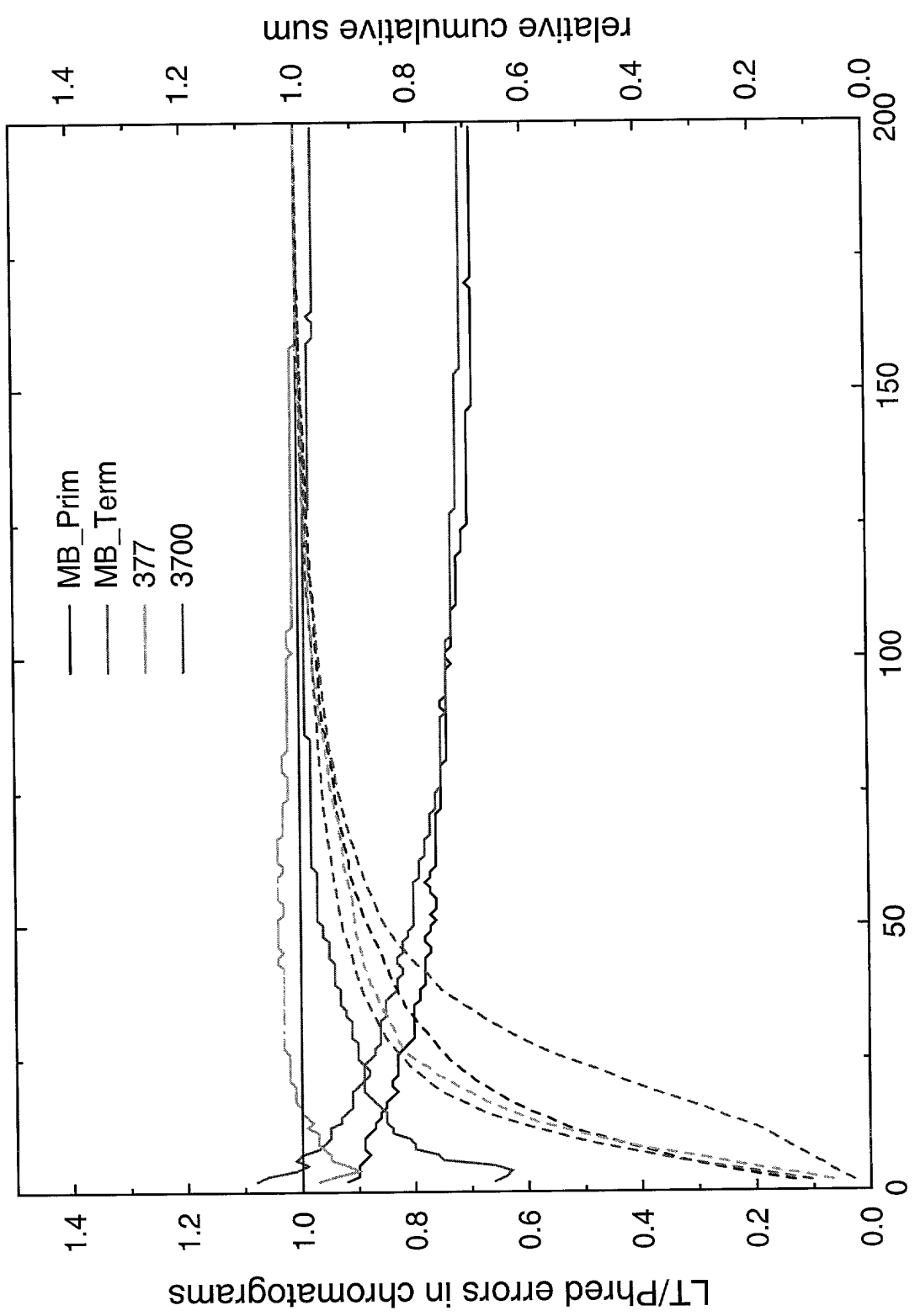
FIG. 7B

C T A A C A C T T C A G I I C T T G A T A G G A A Phred
 C T A C A C I C C A T T C T G A T A G G A A Life
 Trace

260 265 270 275 28

The graph displays a highly variable signal. The y-axis, labeled 'peak distance', ranges from 0 to 40 in increments of 10. The x-axis, labeled 'peak location', ranges from 0 to 10000 in increments of 2000. The signal starts at a low level (around 10-15) for the first 2000 units. Between 2000 and 4000, it fluctuates significantly between 15 and 30. From 4000 to 6000, the signal drops slightly but remains noisy, mostly between 15 and 25. Between 6000 and 8000, it rises to a higher level, fluctuating between 20 and 35. Finally, from 8000 to 10000, it remains at this higher level with continued high-frequency noise.

FIG. 8



x, LT and Phred generate fewer than x errors in chromatogram

FIG. 9

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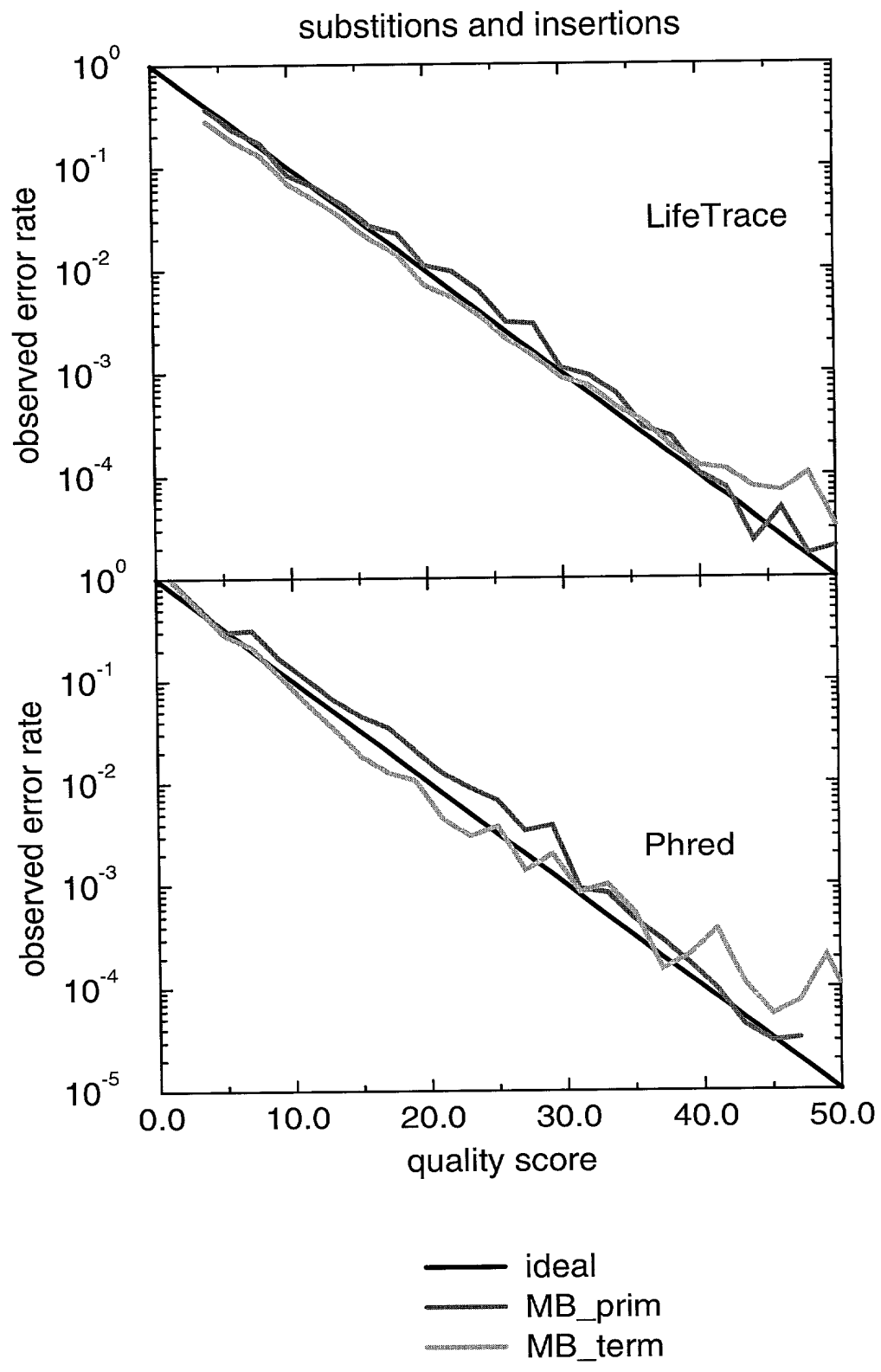


FIG. 10

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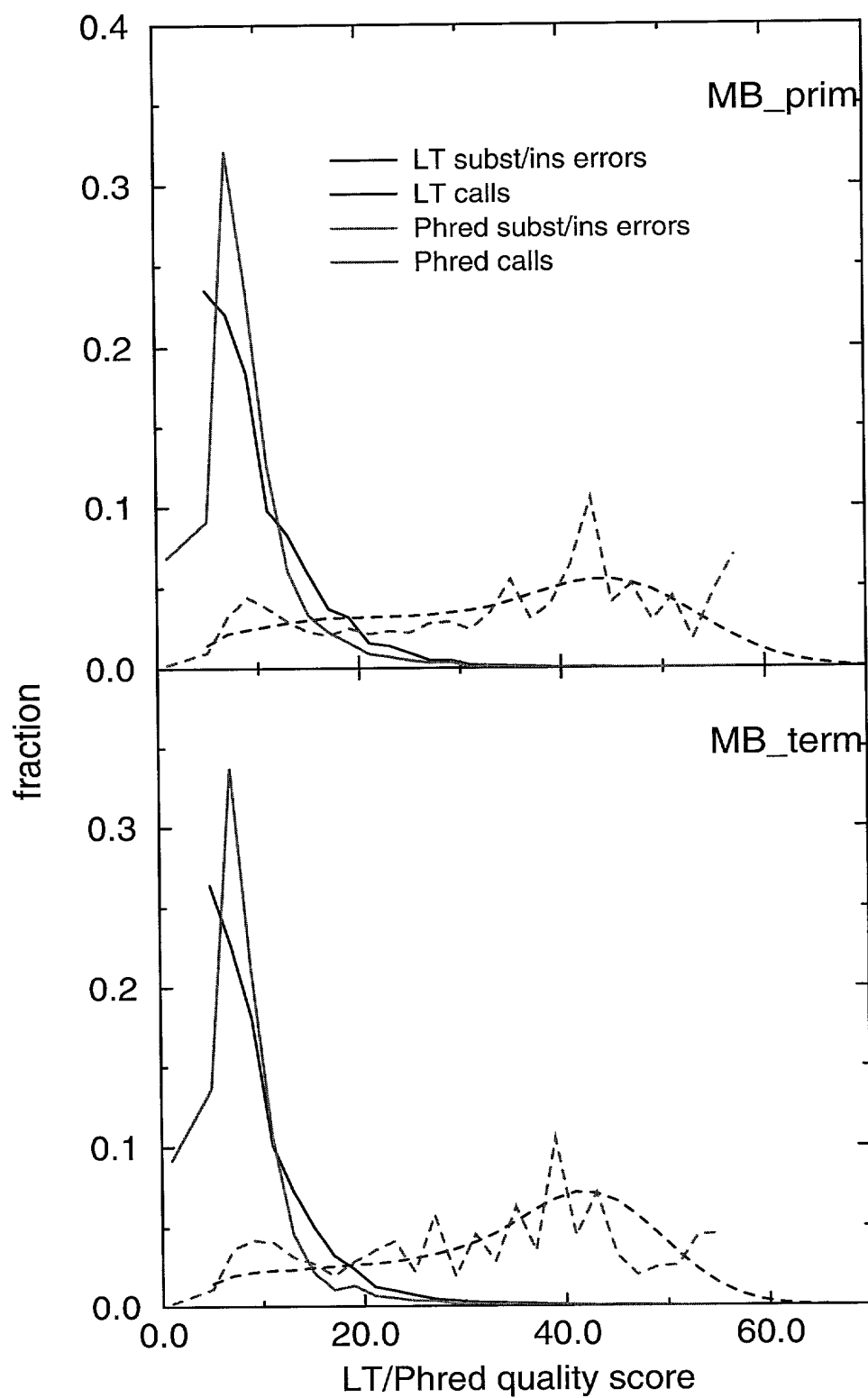


FIG. 11

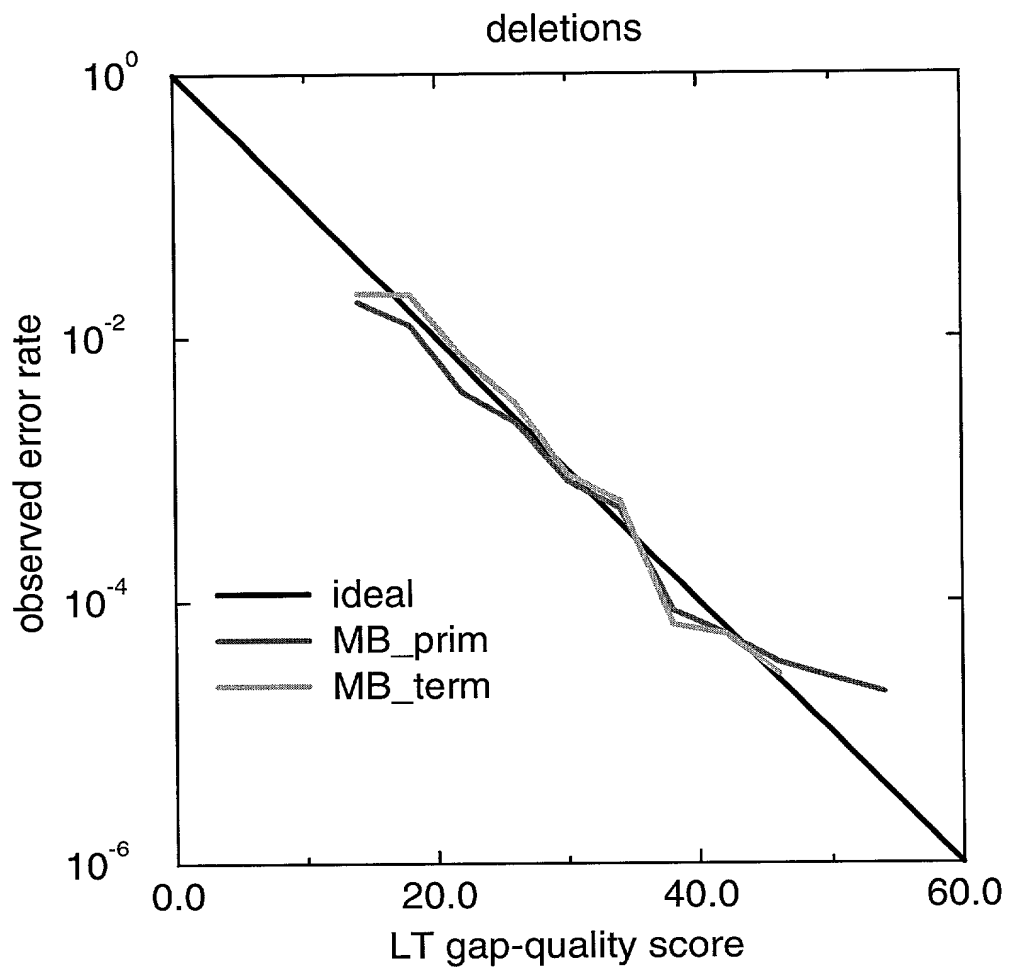


FIG. 12

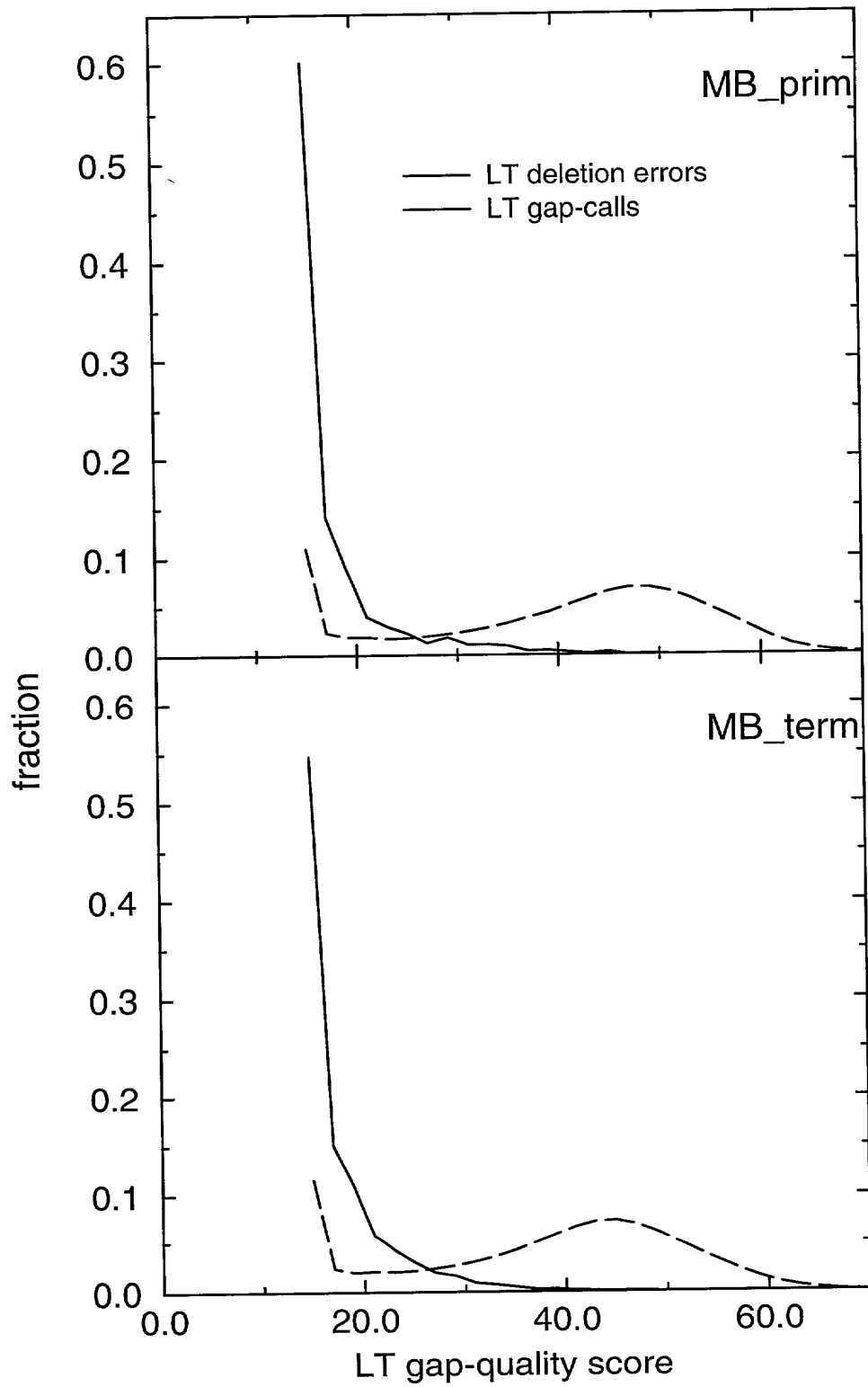


FIG. 13